FBS26- FBU Report Wording

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1. Scope

1.1. The procedures listed below are provided for analysts to use when writing Forensic Biology Unit reports to relay the results and scientifically supported conclusions relative to the testing conducted in as concise a manner as possible.

2. Background

2.1. The content of Forensic Biology Unit laboratory reports must conform to the requirements of the Department of Forensic Sciences (DFS) Forensic Science Laboratory (FSL) Quality Assurance Manual, Forensic Biology Unit (FBU) Quality Assurance Manual, the accreditation standards under ISO/IEC 17025 (current revision), the supplemental standards set by the FSL's accrediting body, and the FBI's Quality Assurance Standards for Forensic DNA Testing Laboratories.

3. Safety

3.1. Not applicable

4. Materials Required

4.1. Not applicable

5. Standards and Controls

5.1. Not applicable

6. Procedures

6.1. In general, FBU reports will contain sections in the following order:

6.1.1. Report name (e.g., Report of Examination, Forensic Biology Unit)

6.1.2. Case information block

6.1.3. Item(s) Submitted

6.1.4. Serological Results and Conclusions (as needed)

6.1.5. Male DNA Screening Results (as needed)

6.1.6. DNA Results, Conclusions and Statistics (as needed)

6.1.7. CODIS (as needed)

6.1.8. Examination Methods

6.1.9. Notes

6.1.10. Disposition of Evidence

6.1.11. Signature block

6.2. Report Name

6.2.1. Enter the correct type of report; the standard report template is “Report of Examination”.

6.2.2. If a report is amended, supplemental or a discontinuation of analysis, the report title is appropriately selected to be “Amended Report of Examination”, “Supplemental Report of Examination” or “Discontinuation of Analysis”.

6.2.3. The second line of the report name is “Forensic Biology Unit”.

6.2.3.1. If issuing a supplemental report, the following is listed under the report/notification title and subtitle:

(See previous report(s) dated {enter date})

6.3. Case Information Block

6.3.1. The case information block will include the following fields:

DFS Case Number:	**Primary Agency:** **Agency Case #:**	**Requesting Agency:** **Agency Case #:**	**Offense:**	**Assignment Date:** Click here to enter a date.	**Report Date:** Click here to enter a date.

6.3.2. The DFS Case Number is pre-assigned.

6.3.3. The default for the Primary Agency and Requesting Agency will be the Metropolitan Police Department. Other agencies may submit evidence or request testing as well. When another agency either submits evidence or requests testing, the Primary Agency and Requesting Agency are updated.

6.3.4. The Offense field will contain the appropriate information obtained from the submission paperwork.

6.3.5. The Assignment Date is the date the request for analysis is assigned to the analyst in JusticeTrax LIMS. If multiple requests are associated with the report, or the request is reassigned prior to the issuance of the report, the earliest date will be reported. The Assignment Date is considered the start of analysis.

6.3.6. The Report Date is a drop-down feature in which the analyst chooses the calendar date of when the report is composed. If any edits are made, the report date will be updated to reflect the last revision date. The Report Date is considered the end of analysis.

6.3.7. If the information is not listed in the submitting paperwork, enter “Not listed”.

6.4. Item(s) submitted

6.4.1. The following statement will appear under the Item(s) Submitted section:

DFS CEU submitted the following item(s) to the laboratory for analysis:

6.4.2. The following table will be filled out for each evidentiary item that was submitted to the FBU:

DFS Item#	Agency Item#	Item Description	DFS Sub-Item#	Sub-Item Description	Examined (Yes/No)
					Select

6.4.2.1. The DFS Item#, Agency Item#, Item Description, DFS Sub-Item# and Sub-Item Description are obtained from the submission paperwork and/or evidence packaging.

6.4.2.2. In the Examined column, there is a drop-down menu with the options “Yes” or “No” to indicate whether the item/sub-item was examined.

6.4.2.3. For any unused fields enter “N/A”.

6.4.2.4. For any unused columns, enter “N/A”, do not delete.

6.4.2.5. Delete any unused rows.

6.5. Serological Results and Conclusions

6.5.1. The following table will be filled out for each evidentiary item/sub-item# that is serologically tested:

Serological Results and Conclusions

DFS Item/Sub-Item#	Item/Sub-Item Description	Blood Results	Semen Results	Processed for DNA
		Select	Select	Select

6.5.2. Enter DFS Item/Sub-Item# and Item/Sub-Item Description. Items such as slides created during differential extraction will be listed at the lowest child level.

6.5.2.1. For differentials: Add (SF) for sperm fraction or (EF) for epithelial fraction at the end of the DFS Item/Sub-Item# and Item/Sub-Item Description columns.

6.5.3. The Blood Results, Semen Results and Processed for DNA columns contain pre-populated statements. Select the appropriate statement from the dropdown.

6.5.4. See section 6.5.7 for the Blood results and section 6.5.8 for Semen results.

6.5.5. In the Processed for DNA column, make a selection from the drop-down menu to indicate whether the item/sub-item was processed for DNA.

6.5.6. If serology was not performed on the case, the entire serology section will be deleted out of the report.

6.5.7. Biological Screening results - testing for blood:

Possible Blood Statements	When to Use
Indicated	Positive Phenolphthalein test result
Not detected	Negative Phenolphthalein test result
Inconclusive	Inconclusive Phenolphthalein test result
Not observed using a visual exam	Item/sub-item is visually negative for the presence of blood
Not tested	Test was not performed on item/sub-item

6.5.8. Biological Screening results - testing for semen:

Possible Semen Statements	**When to Use**
Semen confirmed	Positive microscopic exam and a positive p30 test, any AP result, any ALS result
Seminal fluid confirmed	Microscopic negative or not tested, p30 positive, any AP result, any ALS result
Spermatozoa Identified	Positive microscopic exam, p30 negative or not tested, any AP result, any ALS result
No spermatozoa Identified	Negative microscopic exam, p30 not tested, AP not tested, any ALS result
No semen detected	Negative microscopic exam or not tested, negative testing results for AP and/or p30, any ALS results
Seminal fluid indicated but not confirmed	No microscopic exam performed, AP+, p30 negative or inconclusive, any ALS results
Seminal fluid inconclusive	No microscopic exam performed, AP inconclusive and/or p30 inconclusive, any ALS result
Not observed using a visual exam	Item/sub-item is visually negative and/or ALS negative for staining. No other testing was performed
Not tested	Test was not performed on item/sub-item

6.6. Male DNA Screening Results

6.6.1. The following table will be filled out for each evidentiary item/sub-item that is tested for the presence of male DNA for sexual assault case screening or case scenario dependent.

Male DNA Screening Results

DFS Item/Sub-Item#	Item/Sub-Item Description	Results	Processed for DNA	Reason Sample not Processed for DNA
		Select	Select	Select

6.6.1.1. Enter DFS Item/Sub-Item# (at the lowest child level) and Item/Sub-Item Description.

6.6.1.1.1. Differential extractions should be reported at the fraction level.

6.6.1.1.2. For differentials: Add (SF) for sperm fraction or (EF) for epithelial fraction at the end of the DFS Item/Sub-Item# and Item/Sub-Item Description columns.

6.6.1.2. The Results, Processed for DNA and Reason Sample not Processed for DNA columns contain pre-populated statements for possible results.

6.6.1.3. In the Results column, make a selection from the drop-down menu to indicate whether the item/sub-item is Positive (both human and male DNA detected) or Negative (either of the

following: 1) human DNA detected and no male DNA detected, or 2) no human DNA detected).

6.6.1.4. In the Processed for DNA column, make a selection from the drop-down menu to indicate whether the item/sub-item was processed for DNA.

6.6.1.5. In the Reason Sample not Processed for DNA column, make a selection from the drop-down menu to indicate the reason why the sample was not processed for DNA.

Reason Sample not Processed for DNA	**When to Use**
Other positive sample(s) selected for further DNA testing	Other male DNA positive sample(s) were processed further
Male DNA indicated; however, high levels of total DNA present	Male DNA to Total DNA is < 1:45 (Identifiler Plus) OR Male DNA to Total DNA is < 1:20 (GlobalFiler)
No male DNA detected	The presence of male DNA was not detected
No human DNA detected	The presence of human DNA was not detected
Limited amount of DNA detected, no indication of male	The maximum amount of Total DNA that can be entered into an amplification reaction is < 0.041 ng (Identifiler Plus) and male DNA was not detected OR The maximum amount of Total DNA that can be entered into an amplification reaction is < 0.1 ng (GlobalFiler) and male DNA was not detected
Limited amount of DNA detected, indication of male	The maximum amount of Total DNA that can be entered into an amplification reaction is < 0.041 ng (Identifiler Plus) and male DNA was detected OR The maximum amount of Total DNA that can be entered into an amplification reaction is < 0.1 ng (GlobalFiler) and male DNA was detected
N/A	Sample was processed for DNA

6.6.1.6. If the processing of reference standards is terminated due to the male screening results, the following sentence will remain in the report with the appropriate references listed:

Processing of the following reference standard(s) in this case [Select] terminated prior to STR testing due to the male DNA screening results of the evidence:

6.6.1.6.1. If the processing of reference standards was not terminated, the sentence listed above will be deleted out.

6.7. DNA Results, Conclusions and Statistics

6.7.1. Reference samples will be listed first in this section (if present and tested).

NOTE: Alternate knowns or pseudo-exemplars should be referred to as the item that was submitted for the individual, not as a direct reference from the individual. For example, “cigarette butt from John Doe”.

6.7.1.1. If only one reference sample was tested, the result is listed using the following statement and table:

A DNA profile was obtained from the following reference standard:

DFS Item Number	Name

6.7.1.2. If more than one reference sample was tested, the results are listed using the following statement and table:

DNA profiles were obtained from the following reference standards:

DFS Item Number	Name

6.7.2. Amplification cut-off samples that are not captured in the Male DNA Screening section will be listed next if present.

6.7.2.1. If the maximum amount of total DNA that could be entered into an amplification reaction is <0.041 ng (Identifiler Plus) or <0.1 ng (GlobalFiler), the result(s) are listed using the following statement and table:

Human DNA was detected in the following sample(s); however, [Select] insufficient for conducting the STR DNA testing performed in the laboratory:

DFS Item Number	Item Description

6.7.2.2. For samples that yielded no results during quantitation, the result(s) are listed using the following statement and table:

No human DNA suitable for STR testing was detected in the following sample(s):

DFS Item Number	Item Description

6.7.2.3. For non-male DNA screening samples that are not processed further after quantitation, the following statement and table is used:

Human DNA was detected in the following sample(s); however, [Select] not processed further due to other positive samples being selected for DNA testing:

DFS Item Number	Item Description

6.7.2.4. If the processing of reference standards is terminated due to the human screening results, the following sentence will remain in the report with the appropriate references listed:

Processing of the following reference standard(s) in this case [Select] terminated prior to STR testing due to the human DNA screening results of the evidence:

6.7.2.4.1. *If the processing of reference standards was not terminated, the sentence listed above will be deleted out.*

6.7.3. For reference or evidence samples in which a quality control reason prevents the reporting of results, the following statement, at a minimum, will be used:

Results for the following reference standard(s)/sample(s) will not be reported due to quality control reasons:

DFS Item Number	Item Description/Name

6.7.4. Evidence sample DNA results, reference comparisons and statistics will be listed next if present.

6.7.5. Complete the table listed below for each evidence sample that was processed for STR analysis:

DFS Item/Sub-Item#	Item/Sub-Item Description	Mixture Present	Assumed Number of Contributors	DFS Item#/ Reference Name		Interpretation
		Select	Select			Select
						Select
						Select
Conclusion(s):						

6.7.6. Enter in the DFS Item/Sub-Item# and the Item/Sub-Item Description (at the lowest child level).

6.7.6.1. *Differential extractions should be reported at the fraction level.*

6.7.6.2. *For differentials: Add (SF) for sperm fraction or (EF) for epithelial fraction at the end of the DFS Item/Sub-Item# and Item/Sub-Item Description columns.*

6.7.7. In the Mixture Present column, make a selection from the drop-down menu indicating “Yes” if a mixture is present, “No” if single source or “N/A” if no STR results were obtained or limited data was obtained to determine if sample is a mixture. See FBS21 (ID+ Interpretation) or FBS31 (GlobalFiler Interpretation) on how to determine if a mixture is present.

6.7.8. In the Assumed Number of Contributors column, make the appropriate selection from the drop-down menu. See FBS21 (ID+ Interpretation) or FBS31 (GlobalFiler Interpretation) to determine the number of contributors.

Assumed Number of Contributors	When to Use
1	Profile is determined to be single source.
2	Profile is determined to be from two contributors.
3	Profile is determined to be from three contributors.
4	Profile is determined to be from four contributors.
5 (GlobalFiler only)	Profile is determined to be from five contributors.
2 or 3	Profile is determined to be from either two or three contributors, and a LR comparison was not performed.
2 or 3, reported as 2	Profile is determined to be from either two or three contributors, the profile was run in STRmix as from both two and three contributors. Two contributor LR results reported.

2 or 3, reported as 3	Profile is determined to be from either two or three contributors, the profile was run in STRmix as from both two and three contributors. Three contributor LR results reported.
3 or 4	Profile is determined to be from either three or four contributors and a LR comparison was not performed.
3 or 4, reported as 3	Profile is determined to be from either three or four contributors, the profile was run in STRmix as from both three and four contributors. Three contributor LR results reported.
3 or 4, reported as 4	Profile is determined to be from either three or four contributors, the profile was run in STRmix as from both three and four contributors. Four contributor LR results reported.
4 or 5 (GlobalFiler only)	Profile is determined to be from either four or five contributors and a LR comparison was not performed.
4 or 5, reported as 4 (GlobalFiler only)	Profile is determined to be from either four or five contributors, the profile was run in STRmix as from both four and five contributors. Four contributor LR results reported.
4 or 5, reported as 5 (GlobalFiler only)	Profile is determined to be from either four or five contributors, the profile was run in STRmix as from both four and five contributors. Five contributor LR results reported.
Uninterpretable-Complexity of mixture (Identifiler Plus)	Profile is determined to be from either four or five contributors. OR Profile is determined to be from more than four contributors. OR The number of contributors is not able to be determined due to potential allele sharing, such as in the case of closely related family members.
Uninterpretable-Complexity of mixture (GlobalFiler)	Profile is determined to be from either five or six contributors. OR Profile is determined to be from more than five contributors. OR The number of contributors is not able to be determined due to potential allele sharing, such as in the case of closely related family members.
Uninterpretable-Limited data obtained	Not enough data present in profile to determine number of contributors.
N/A	No results obtained.

6.7.9. In the DFS Item#/Reference Name column, list each reference that was processed for STR analysis and the respective item number if applicable.

6.7.9.1. If no references are available, type N/A in the DFS Item #/Reference Name and Interpretation sections.

6.7.10. In the Interpretation column, select the appropriate qualitative comparison statement from the drop-down menu.

Interpretation	**When to Use**
Included	Qualitative comparison of data between the reference sample profile and the evidence sample profile indicates they are consistent with each other
Excluded	Qualitative comparison of data between the reference sample profile and the evidence sample profile indicates they are not consistent with each other
Inconclusive	There is not enough data to support a qualitative inclusion or exclusion
N/A- No results obtained	No STR results were obtained from the evidence sample; therefore, no reference comparison can be made
N/A- Uninterpretable	STR results are uninterpretable due to limited data or complexity of mixture; therefore, no reference comparisons can be made

6.7.10.1. If a qualitative exclusion is made, a likelihood ratio will not be calculated.

6.7.10.2. A statistical calculation will be performed for all probative inclusionary and inconclusive qualitative comparison statements. Results will be reported to 3 digits. (See section 6.7.11 for Likelihood Ratio statements).

6.7.11. The Conclusion(s) section is used for the reporting of unknown profiles (including deconvolutions obtained from STRmix), and Likelihood Ratio (LR) statements, if applicable.

6.7.11.1. Statements regarding the evidence sample will be listed before LR statements.

6.7.11.2. Single source profile statements

6.7.11.2.1. If a single source profile is consistent with a non-probative reference (i.e., victim reference, elimination reference), no statement is needed in the Conclusion(s) section.

6.7.11.2.2. If a single source profile is not consistent with a non-probative reference sample or if no reference sample was submitted, the Conclusion(s) section will include an appropriate statement that a profile was obtained.

6.7.11.2.3. If no reference sample was submitted, include the following statement:

A comparison may be performed with the submission of a reference standard.

6.7.11.3. Mixture profile statements

6.7.11.3.1. If a contributor(s) is assumed in a mixture, the following statements will be used:

The following individual is expected to be present in the mixture and is an assumed contributor:

Or:

The following individuals are expected to be present in the mixture and are assumed contributors:

6.7.11.3.1.1. If there are no assumed contributors, this statement will be deleted.

6.7.11.3.2. If no reference sample was submitted, include the following statement:

A comparison may be performed with the submission of a reference standard.

6.7.11.4. Delete any unused statements.

6.7.12. Likelihood Ratio Statements

6.7.12.1. The likelihood ratio is a numerical value. A likelihood ratio will be generated for every evidence item/sub-item where appropriate. If the profiles generated are the same, the overall lowest LR from the four (GlobalFiler) or three (Identifiler Plus) population groups (most conservative) using the conservative lower bound of the HPD interval will be reported. The DFS Item/Sub-Item numbers can be entered in the same block along with the corresponding sample description.

6.7.12.2. For single source Identifiler Plus and GlobalFiler samples where there is a probative inclusion for a reference sample, the following statement will be used:

The DNA profile obtained from the evidence item listed above is at least XXX times more likely if it originated from REFERENCE (ITEM #) than if it originated from an unknown, unrelated individual.

6.7.12.3. For Identifiler Plus and GlobalFiler mixtures where the LR > 1, the following statement will be used:

The mixture DNA profile obtained from the evidence item listed above is at least XXX times more likely if it originated from REFERENCE (Item #) and REFERENCE (Item #) and/or XXX unknown, unrelated individual(s) than if it originated from any assumed contributors and XXX unknown, unrelated individuals.

6.7.12.4. For Identifiler Plus and GlobalFiler mixtures where the LR < 1, the following statement will be used:

The mixture DNA profile obtained from the evidence item listed above is at least YYY times more likely if it originated from any assumed contributors and XXX unknown, unrelated individuals than if it originated from REFERENCE (Item #) and REFERENCE (Item #) and/or XXX unknown, unrelated individual(s).

NOTE: YYY = 1/LR

6.7.12.5. For Identifiler Plus and GlobalFiler mixtures where the LR = 0, the following statement will be used:

REFERENCE (Item #) is excluded as a contributor to the evidence item listed above.

6.7.12.6. For Identifiler Plus and GlobalFiler mixtures where the LR = 1.00, the following statement will be used:

There is equal support for REFERENCE (Item #) to be included and excluded as contributor(s) to the mixture DNA profile obtained from the item listed above.

6.7.12.7. For all non-zero LRs, a verbal equivalent statement associated with the LR value will be included and selected from the drop-down menu illustrated below:

This is Choose an item. for the following individual(s) to be Choose an item. as contributor(s) to the DNA profile obtained from the item listed above:

See Notes section for verbal scale.

6.7.12.8. There may be certain instances in which multiple pairs of propositions are run in STRmix. See FBS31- GlobalFiler

Interpretation and FBS21- ID+ Interpretation. In this situation, the following statement will be included:

There are other pairs of propositions that were considered in this instance resulting in different likelihood ratios. See casefile for additional information.

NOTE: This statement does not apply to a profile run through STRmix under two different contributor numbers, as this information is contained in the "Assumed Number of Contributors" column of the evidence sample table.

6.8. CODIS

6.8.1. One of the two CODIS statements listed below will be included in each report:

6.8.1.1. *A CODIS eligible profile was obtained from Item Description (Item #) and was entered into CODIS, in accordance with local and national regulations, to be maintained for routine searching. If a CODIS hit occurs, you will be notified via a CODIS Hit Notification letter upon confirmation of the hit. Notification will be provided if the profile is removed from CODIS at any point in the future*

6.8.1.2. *No CODIS eligible profile(s) were obtained.*

6.8.2. For non-DNA cases and discontinuation reports, a CODIS statement is not included.

6.9. Examination Methods

6.9.1. A list of examination methods used is pre-populated in the report template. All that do not apply should be removed.

6.10. Notes

6.10.1. A notes section is included in each report to help with any clarification.

6.10.2. If a non-zero likelihood ratio is calculated, a verbal scale is included in this section. See below for full verbal scale published in the Forensic Biology Report.

Likelihood Ratio Verbal Equivalent Scale					
1,000,000	≤	LR or 1/LR			Very strong support
10,000	≤	LR or 1/LR	<	1,000,000	Strong support
100	≤	LR or 1/LR	<	10,000	Moderate support
1	<	LR or 1/LR	<	100	Limited support
1	=	LR			Uninformative

From *Recommendations of the SWGDAM Ad Hoc Working Group on Genotyping Results Reported as Likelihood Ratios, pg. 3 (2018)*

6.10.3. Any additional information deemed necessary by the analyst will be included in this section of the report.

6.11. Disposition

6.11.1. The following disposition statement will be included in each report:

It is FSL policy to return evidence received, and items collected and preserved, to DFS CEU after the Technical Review. DNA extracts are retained by the Forensic Biology Unit.

6.12. Signature

6.12.1. At the end of the report, the reporting analyst is required to sign the report. Below the signature, the reporting analyst's name is printed along with his/her title.

7. Sampling

7.1. Not applicable

8. Calculations

8.1. Not applicable

9. Uncertainty of Measurement

9.1. Not applicable

10. Limitations

10.1. It is not possible to anticipate the nature of all potential DNA typing results, or the nature of the evidentiary samples from which they may be obtained. These procedures do not exhaust the possible list of the results that may be encountered by the analyst nor the conclusions that the analyst may render based on their interpretation of those results. For results not specifically

described, conclusion statements should be drafted using statements above that are similar in concept and/or origin, with Technical leader approval.

10.2. Not every situation can, or should, be covered by a pre-set reporting statement. It is important that the analyst follows interpretation criteria for a test when reporting examination results and conclusions.

10.3. Any report statements listed herein are intended as a guide only.

11. Documentation

11.1. FBU Report of Examination

12. References

12.1. ISO/IEC 17025 – General Requirements for the Competence of Testing and Calibration Laboratories, International Organization for Standardization, Geneva, Switzerland (Current Revision)

12.2. Federal Bureau of Investigation, Quality Assurance Standards for Forensic DNA Testing Laboratories (Current Revision)

12.3. National Research Council. The Evaluation of Forensic DNA Evidence, Washington, D.C.: National Academy Press, 1996

12.4. SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories (2017 Revision)

12.5. Recommendations of the SWGDAM Ad Hoc Working Group on Genotyping Results Reported as Likelihood Ratios (2018)

12.6. LOM02 – Practices for Case Documentation and Report Writing

12.7. FBS21 – Identifiler Plus Interpretation

12.8. FBS31 – GlobalFiler™ Interpretation

12.9. FBS25 – Data Analysis Using STRmix™

12.10. Forensic Science Laboratory Quality Assurance Manual

12.11. Forensic Biology Unit Quality Assurance Manual

12.12. FBS32 – GlobalFiler Data Analysis Using STRmix™